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1642

RAW SEQUENCE LISTING

DATE: 07/12/2002

PATENT APPLICATION: US/09/674,035A

TIME: 10:40:08

Input Set : A:\227274078.ST25.txt

Output Set: N:\CRF3\07122002\I674035A.raw

3 <110> APPLICANT: Lang, Jas C.
 5 <120> TITLE OF INVENTION: Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

7 <130> FILE REFERENCE: 22727/04078
 9 <140> CURRENT APPLICATION NUMBER: 09/674,035A
 10 <141> CURRENT FILING DATE: 2000-12-11
 12 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01818
 13 <151> PRIOR FILING DATE: 1999-11-11
 15 <160> NUMBER OF SEQ ID NOS: 10
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1269
 21 <212> TYPE: DNA
 22 <213> ORGANISM: DESC1
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1269)
 27 <223> OTHER INFORMATION:
 30 <400> SEQUENCE: 1

ENTERED

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| 32 Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu | |
| 33 1 5 10 15 | |
| 35 ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca | 96 |
| 36 Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala | |
| 37 20 25 30 | |
| 39 gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag | 144 |
| 40 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys | |
| 41 35 40 45 | |
| 43 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat | 192 |
| 44 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr | |
| 45 50 55 60 | |
| 47 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag | 240 |
| 48 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln | |
| 49 65 70 75 80 | |
| 51 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg | 288 |
| 52 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg | |
| 53 85 90 95 | |
| 55 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat | 336 |
| 56 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His | |
| 57 100 105 110 | |
| 59 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag | 384 |
| 60 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu | |
| 61 115 120 125 | |
| 63 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag | 432 |

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64 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
65      130                      135                      140
67 ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa      480
68 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
69 145                      150                      155                      160
71 att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc      528
72 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
73                      165                      170                      175
75 tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt      576
76 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
77                      180                      185                      190
79 ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg      624
80 Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
81      195                      200                      205
83 cag tgg gat ggg agt cat gcg tgt gga gca acc tta att aat gcc aca      672
84 Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
85      210                      215                      220
87 tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc      720
88 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
89 225                      230                      235                      240
91 aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa      768
92 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
93                      245                      250                      255
95 cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca      816
96 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
97                      260                      265                      270
99 cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac      864
100 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
101      275                      280                      285
103 aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt      912
104 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
105      290                      295                      300
107 caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat      960
108 Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
109 305                      310                      315                      320
111 gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata      1008
112 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
113                      325                      330                      335
115 gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act      1056
116 Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
117                      340                      345                      350
119 cct aga atc tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc      1104
120 Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
121                      355                      360                      365
123 cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc      1152
124 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
125      370                      375                      380
127 tgg tac ctt gct gga ata gtg agc tgg gga gat gaa tgt gcg aaa ccc      1200
128 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro

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129 385          390          395          400
131 aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att      1248
132 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
133          405          410          415
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140 <210> SEQ ID NO: 2
141 <211> LENGTH: 422
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143 <213> ORGANISM: DESC1
145 <400> SEQUENCE: 2
147 Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
148 1          5          10          15
151 Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala
152          20          25          30
155 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
156          35          40          45
159 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
160          50          55          60
163 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
164 65          70          75          80
167 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
168          85          90          95
171 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
172          100          105          110
175 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
176          115          120          125
179 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
180          130          135          140
183 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
184 145          150          155          160
187 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
188          165          170          175
191 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
192          180          185          190
195 Gly Gly Thr Glu Val Glu Glu Gly Trp Pro Trp Gln Ala Ser Leu
196          195          200          205
199 Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
200          210          215          220
203 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
204 225          230          235          240
207 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
208          245          250          255
211 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
212          260          265          270
215 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
216          275          280          285
219 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe

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220      290      295      300
223 Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
224 305      310      315      320
227 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
228      325      330      335
231 Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
232      340      345      350
235 Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
236      355      360      365
239 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
240      370      375      380
243 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
244 385      390      395      400
247 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
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251 Thr Ser Lys Thr Gly Ile
252      420
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 1269
257 <212> TYPE: DNA
258 <213> ORGANISM: DESC1
260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (1)..(1269)
263 <223> OTHER INFORMATION:
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268 Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
269 1      5      10      15
271 ccc tgg gtt atc ggc ctc gtc atg ttc ata tcc ctg att gtc ctg gca      96
272 Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
273      20      25      30
275 gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag      144
276 Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
277      35      40      45
279 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat      192
280 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
281      50      55      60
283 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag      240
284 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
285 65      70      75      80
287 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg      288
288 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
289      85      90      95
291 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat      336
292 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
293      100      105      110
295 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag      384
296 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu

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| 297 | 115 | 120 | 125 | |
| 299 | gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag | 432 | | |
| 300 | Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys | | | |
| 301 | 130 | 135 | 140 | |
| 303 | ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa | 480 | | |
| 304 | Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys | | | |
| 305 | 145 | 150 | 155 | 160 |
| 307 | att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc | 528 | | |
| 308 | Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys | | | |
| 309 | 165 | 170 | 175 | |
| 311 | tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt | 576 | | |
| 312 | Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val | | | |
| 313 | 180 | 185 | 190 | |
| 315 | ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg | 624 | | |
| 316 | Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu | | | |
| 317 | 195 | 200 | 205 | |
| 319 | cag tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca | 672 | | |
| 320 | Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr | | | |
| 321 | 210 | 215 | 220 | |
| 323 | tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc | 720 | | |
| 324 | Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala | | | |
| 325 | 225 | 230 | 235 | 240 |
| 327 | aga tgg act gct tcc ttt gga gta aca ata aaa cct tgc aaa atg aaa | 768 | | |
| 328 | Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys | | | |
| 329 | 245 | 250 | 255 | |
| 331 | cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca | 816 | | |
| 332 | Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser | | | |
| 333 | 260 | 265 | 270 | |
| 335 | cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac | 864 | | |
| 336 | His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr | | | |
| 337 | 275 | 280 | 285 | |
| 339 | aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt | 912 | | |
| 340 | Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe | | | |
| 341 | 290 | 295 | 300 | |
| 343 | caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat | 960 | | |
| 344 | Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn | | | |
| 345 | 305 | 310 | 315 | 320 |
| 347 | gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata | 1008 | | |
| 348 | Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile | | | |
| 349 | 325 | 330 | 335 | |
| 351 | gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act | 1056 | | |
| 352 | Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr | | | |
| 353 | 340 | 345 | 350 | |
| 355 | cct aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc | 1104 | | |
| 356 | Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys | | | |
| 357 | 355 | 360 | 365 | |
| 359 | cag ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc | 1152 | | |
| 360 | Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile | | | |
| 361 | 370 | 375 | 380 | |

VERIFICATION SUMMARY

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